

1. *Chlorophytum comosum* (L.) Willd. var. *spicatum* (L.) Kuntze

10. The following table shows the number of hours worked by each employee.

W. C. G. - 1910

10 *Journal of Health Politics, Policy and Law*, Vol. 30, No. 1, January 2005

$\frac{1}{2} \pi - \theta = \frac{1}{2} \pi - \alpha + \beta$ or $\theta = \alpha - \beta$.

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卷之三

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14) P1776R2 and p1776R1 have identical amino acid sequences up to 44
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the first time that I have ever seen a bird of this species.

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1996-1997 学年第二学期期中考试卷

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ANSWER

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mitochondrial DNA

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100-17

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40 1111 111

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Chin. J. Chem.

it's got it

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2.2.2. DNA

113

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www.elsevier.com

Sequence Listing

<110> Gerritsen, Mary E.

Goddard, Audrey

Grimaldi, J. Christopher

Mehraban, Fuad

<120> NOVEL POLYPEPTIDES, THEIR NUCLEIC ACIDS, AND METHODS
FOR THEIR USE IN ANGIOGENESIS AND VASCULARIZATION

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Glu Tyr Ile Ile Arg Val Gln Arg Gly Ile Ser Val Glu
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Asp Lys Asp Phe Gln Cys Leu Ile Lys Leu Leu Pro Ser
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aag gga ttc cct tat ggg cat ctt cac gcc tcc aat gtg 947
Lys Gly Phe Pro Tyr Gly His Leu His Ala Ser Asn Val
285 290

atg ctc gat ggg gac act tgc cgg ctg ctc gac ctt gag 986
Met Leu Asp Gly Asp Thr Cys Arg Leu Leu Asp Leu Glu
295 300 305

aat tcc tta ttg ggc ctg cct tcc ttc tac cga tct tat 1025
Asn Ser Leu Leu Gly Leu Pro Ser Phe Tyr Arg Ser Tyr
310 315 320

ttt tca caa ttc aqq aaa atc aat aca ttq qaa agt gtg 1064
Phe Ser Gln Phe Arg Lys Ile Asn Thr Leu Glu Ser Val
325 330

gat gtc cac tgc ttt ggc cac tta ctg tat gaa atg act 1103
Asp Val His Cys Phe Gly His Leu Leu Tyr Glu Met Thr
335 340 345

tat gga cga ccg cca gac tgc gtg cct gtg gac tcc ttc 1142
Tyr Gly Arg Pro Pro Asp Ser Val Pro Val Asp Ser Phe
350 355

cct cct gcc ccg tcc atg gct gtg gtg gcc gtg ttg gag 1181
Pro Pro Ala Pro Ser Met Ala Val Val Ala Val Leu Glu
360 365 370

tct acg ctg tct tgt gaa gcc tgt aaa aat ggc atg cct 1220
Ser Thr Leu Ser Cys Glu Ala Cys Lys Asn Gly Met Pro
375 380 385

acc atc tcc cgg ctc tta cag atg cca tta ttc agc gat 1259
Thr Ile Ser Arg Leu Leu Gln Met Pro Leu Phe Ser Asp
390 395

gtt tta cta acc act tct gaa aaa cca cag ttt aag atc 1298
Val Leu Leu Thr Ser Glu Lys Pro Gln Phe Lys Ile
400 405 410

cct aca aag tta aaa gag gca ttg aga att gcc aaa gaa 1337
Pro Thr Lys Leu Lys Glu Ala Leu Arg Ile Ala Lys Glu
415 420

tgt ata gag aag aga cta att gag gaa cag aaa cag att 1376
Cys Ile Glu Lys Arg Leu Ile Glu Glu Gln Lys Gln Ile
425 430 435

cac cag cat cga aga ctg aca aga gct cag tcc cac cat 1415
His Gln His Arg Arg Leu Thr Arg Ala Gln Ser His His
440 445 450

gga tct gag gag gaa aga aaa aaa aga aag att tta gct 1454
Gly Ser Glu Glu Arg Lys Lys Arg Lys Ile Leu Ala
455 460

cga aag aag tca aaa cga tct gct ctt gaa aat agt gaa 1493
Arg Lys Lys Ser Lys Arg Ser Ala Leu Glu Asn Ser Glu
465 470 475

gag cat tca gcg agg tac agc aac tcc aat aat tca gga 1532
Glu His Ser Ala Arg Tyr Ser Asn Ser Asn Asn Ser Gly
480 485

tct ggg gcc agc tca cct ctc acg tcc cgg tca tcg cca 1571

Ser Gly Ala Ser Ser Pro Leu Thr Ser Pro Ser Ser Pro
490 495 500

act cca ccc tat aca tca ggg ata tct gca tta cct cca 1610
Thr Pro Pro Ser Thr Ser Gly Ile Ser Ala Leu Pro Pro
505 510 515

cct cct cca cct cca cca gca gct ccc ttg cct 1649
Pro Pro Pro Pro Pro Pro Ala Ala Pro Leu Pro
520 525

cct gcg agc acc gag gta cct gcc cag ctc tcg tct caq 1688
Pro Ala Ser Thr Glu Val Pro Ala Gln Leu Ser Ser Gln
530 535 540

gct gtg aat ggc atg agc cga gqq qcc ttg ctc agc tcc 1727
Ala Val Asn Gly Met Ser Arg Gly Ala Leu Leu Ser Ser
545 550

atc cag aat ttc caa aaa gga act ttg agg aaa gcc aaa 1766
Ile Gln Asn Phe Gln Lys Gly Thr Leu Arg Lys Ala Lys
555 560 565

acc tgt gat cac agt gct ccg aag atc ggc tg aa 1800
Thr Cys Asp His Ser Ala Pro Lys Ile Gly
570 575 577

gcttcctgtt tacacttgga gggaaaaagtt cttttttatt cctactcacc 1850
cctacccccc aaactaccct cttcctggga aagtaattgc tgagccagta 1900
cagccacaaa cagtactatt ttgcagatgc tcatgtaagc agctttcga 1950
gagaaataat tcttaagca gaataaagtt aggctggcat tgctccctta 2000
agatcttgct cctttattaa ccctgtaaag gagtcttggt tatacctctaa 2050
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attcaagtac acacatcagt gttggttact atgcagagaa tgtcattgtg 2800

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<211> 577

<212> PRT

<213> Homo sapiens

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Gln Ser His Thr Glu Tyr Ile Ile Arg Val Gln Arg Gly Ile Ser
35 40 45

Val Glu Asn Ser Trp Gln Ile Val Arg Arg Tyr Ser Asp Phe Asp
50 55 60

Leu Leu Asn Asn Ser Leu Gln Ile Ala Gly Leu Ser Leu Pro Leu
65 70 75

Pro Pro Lys Lys Leu Ile Gly Asn Met Asp Arg Glu Phe Ile Ala
80 85 90

Glu Arg Gln Lys Gly Leu Gln Asn Tyr Leu Asn Val Ile Thr Thr
95 100 105

Asn His Ile Leu Ser Asn Cys Glu Leu Val Lys Lys Phe Leu Asp
110 115 120

Pro Asn Asn Tyr Ser Ala Asn Tyr Thr Glu Ile Ala Leu Gln Gln
125 130 135

Val Ser Met Phe Phe Arg Ser Glu Pro Lys Trp Glu Val Val Glu
140 145 150

Pro Leu Lys Asp Ile Gly Trp Arg Ile Arg Lys Lys Tyr Phe Leu
155 160 165

Met Lys Ile Lys Asn Gln Pro Lys Glu Arg Leu Val Leu Ser Trp
170 175 180

Ala Asp Leu Gly Pro Asp Lys Tyr Leu Ser Asp Lys Asp Phe Gln
185 190 195

Cys Leu Ile Lys Leu Leu Pro Ser Cys Leu His Pro Tyr Ile Tyr
200 205 210

Arg Val Thr Phe Ala Thr Ala Asn Glu Ser Ser Ala Leu Leu Ile
215 220 225

Arg Met Phe Asn Glu Lys Gly Thr Leu Lys Asp Leu Ile Tyr Lys
230 235 240

Ala Lys Pro Lys Asp Pro Phe Leu Lys Lys Tyr Cys Asn Pro Lys
245 250 255

Lys Ile Gln Gly Leu Glu Leu Gln Gln Ile Lys Thr Tyr Gly Arg
260 265 270

Gln Ile Leu Glu Val Leu Lys Phe Leu His Asp Lys Gly Phe Pro
275 280 285

Tyr Gly His Leu His Ala Ser Asn Val Met Leu Asp Gly Asp Thr
290 295 300

Cys Arg Leu Leu Asp Leu Glu Asn Ser Leu Leu Gly Leu Pro Ser
305 310 315

Phe Tyr Arg Ser Tyr Phe Ser Gln Phe Arg Lys Ile Asn Thr Leu
320 325 330

Glu Ser Val Asp Val His Cys Phe Gly His Leu Leu Tyr Glu Met
335 340 345

Thr Tyr Gly Arg Pro Pro Asp Ser Val Pro Val Asp Ser Phe Pro
350 355 360

Pro Ala Pro Ser Met Ala Val Val Ala Val Leu Glu Ser Thr Leu
365 370 375

Ser Cys Glu Ala Cys Lys Asn Gly Met Pro Thr Ile Ser Arg Leu
380 385 390

Leu Gln Met Pro Leu Phe Ser Asp Val Leu Leu Thr Thr Ser Glu
395 400 405

Lys Pro Gln Phe Lys Ile Pro Thr Lys Leu Lys Glu Ala Leu Arg
410 415 420

Ile Ala Lys Glu Cys Ile Glu Lys Arg Leu Ile Glu Glu Gln Lys
425 430 435

Gln Ile His Gln His Arg Arg Leu Thr Arg Ala Gln Ser His His
440 445 450

Gly Ser Glu Glu Glu Arg Lys Lys Arg Lys Ile Leu Ala Arg Lys
455 460 465

Lys Ser Lys Arg Ser Ala Leu Glu Asn Ser Glu Glu His Ser Ala
470 475 480

Arg Tyr Ser Asn Ser Asn Asn Ser Gly Ser Gly Ala Ser Ser Pro
485 490 495

Leu Thr Ser Pro Ser Ser Pro Thr Pro Pro Ser Thr Ser Gly Ile
500 505 510

Ser Ala Leu Pro Pro Pro Pro Pro Pro Pro Pro Ala Ala
515 520 525

Pro Leu Pro Pro Ala Ser Thr Glu Val Pro Ala Gln Leu Ser Ser

530	535	540
Gln Ala Val Asn Gly Met Ser Arg Gly Ala Leu Leu Ser Ser Ile		
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Gln Asn Phe Gln Lys Gly Thr Leu Arg Lys Ala Lys Thr Cys Asp		
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His Ser Ala Pro Lys Ile Gly		
575		

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gtgaacatag atacagctct ttccccttcc cccccctttt aaatgtaaca 150
aatactttt atgttcccct tcccccccttcc cccttttccc ctcccccctt 200
ttggaaacgt gtcaggaacc aaatagttt agatgagcag ttgaggggac 250
tgagagagt atcgacacag aacctggctt ctgcgtgctt catcataagt 300
cgtgctgccg gccaggttac ttaagcaccc ttttaacaag gaaaccttgt 350
gggagatcca gctggccgac tcgagttcag aaacaggacc acagaggtt 400
cactctggga tcctggccat gaggttggat gcctcacctt actgaaaagga 450
gacactggac ctaa atg gcg cag cat gat ttt gtt cct gct 491
Met Ala Gln His Asp Phe Val Pro Ala
1 5

tgg cta aat ttc tca aca cca cag tca gct aag tca cct 530
Trp Leu Asn Phe Ser Thr Pro Gln Ser Ala Lys Ser Pro
10 15 20

act gcc acc ttc gaa aaa cac gga gag cac cta ccc aga 569
Thr Ala Thr Phe Glu Lys His Gly Glu His Leu Pro Arg
25 30 35

gga gaa ggt aga ttt gga gta agc cgc cgt cga cat aat 608
Gly Glu Gly Arg Phe Gly Val Ser Arg Arg Arg His Asn
40 45

tcc tct gat ggt ttt aac aat ggt ccc cta cga act 647
Ser Ser Asp Gly Phe Phe Asn Asn Gly Pro Leu Arg Thr
50 55 60

gca gga gat tct tgg cac cag ccc tcc tgt tcc gcc atg 686
Ala Gly Asp Ser Trp His Gln Pro Ser Cys Ser Ala Met
65 70

att ctg tgg act ctg gtg tct cta agg gag cat atg ctg 725
Ile Leu Trp Thr Leu Val Ser Leu Arg Glu His Met Leu

75

80

85

gaa tca cag gga acc cat ctg gtt ggc ata gct ctt ccc 764
 Glu Ser Gln Gly Thr His Leu Val Gly Ile Ala Leu Pro
 90 95 100

cga cgt cat gat ggc atq agc caa cgt agt gta ggt ggc 803
 Arg Gly His Asp Gly Met Ser Gln Arg Ser Val Gly Gly
 105 110

aca ggg aac cat cgc cat tgg aat ggc agc ttc cac tcc 842
 Thr Gly Asn His Arg His Trp Asn Gly Ser Phe His Ser
 115 120 125

cgg aaa ggg tgt gct ttt cag gaa aag cca cct atg gag 881
 Arg Lys Gly Cys Ala Phe Gln Glu Lys Pro Pro Met Glu
 130 135

att agg gaa gaa aag aaa gaa gac aag gtg gaa aag ttg 920
 Ile Arg Glu Glu Lys Lys Glu Asp Lys Val Glu Lys Leu
 140 145 150

cag ttt gaa gag gag gac ttt cct tcc ttg aat cca gaa 959
 Gln Phe Glu Glu Asp Phe Pro Ser Leu Asn Pro Glu
 155 160 165

gct ggc aaa cag cat cag cca tgc aga cct att ggg aca 998
 Ala Gly Lys Gln His Gln Pro Cys Arg Pro Ile Gly Thr
 170 175

cct tct gga gta tgg gaa aac ccg cct agt gcc aag caa 1037
 Pro Ser Gly Val Trp Glu Asn Pro Pro Ser Ala Lys Gln
 180 185 190

ccc tcc aag atg cta gtt atc aaa aaa gtt tcc aaa gag 1076
 Pro Ser Lys Met Leu Val Ile Lys Val Ser Lys Glu
 195 200

gat cct gct gct gcc ttc tct gct gca ttc acc tca cca 1115
 Asp Pro Ala Ala Phe Ser Ala Ala Phe Thr Ser Pro
 205 210 215

gga tct cac cat gca aat ggg aac aaa ttg tca tcc gtg 1154
 Gly Ser His His Ala Asn Gly Asn Lys Leu Ser Ser Val
 220 225 230

gtt cca agt gtc tat aag aac ctg gtt cct aag cct gta 1193
 Val Pro Ser Val Tyr Lys Asn Leu Val Pro Lys Pro Val
 235 240

cca cct cct tcc aag cct aat gca tgg aaa gct aac agg 1232
 Pro Pro Pro Ser Lys Pro Asn Ala Trp Lys Ala Asn Arg
 245 250 255

atg gag cac aag tca gga tcc ctt tcc tct agc cgg gag 1271
 Met Glu His Lys Ser Gly Ser Leu Ser Ser Ser Arg Glu
 260 265

tct gct ttt acc agt cca atc tcc gtt acc aaa cca gtg 1310
 Ser Ala Phe Thr Ser Pro Ile Ser Val Thr Lys Pro Val
 270 275 280

gta ctg gct agt ggt gca gct ctg agt tct ccc aaa gag 1349
Val Leu Ala Ser Gly Ala Ala Leu Ser Ser Pro Lys Glu
285 290 295

agt ccc tcc ayc acc acc cct cca att gag atc ayc tcc 1388
Ser Pro Ser Ser Thr Thr Pro Pro Ile Glu Ile Ser Ser
300 305

tct cgt ctg acc aag ttg acc cgc cga acc acc gac agy 1427
Ser Arg Leu Thr Lys Leu Thr Arg Arg Thr Thr Asp Arg
310 315 320

aag agt gag ttc ctg aaa act ctg aag gat gac cgg aat 1466
Lys Ser Glu Phe Leu Lys Thr Leu Lys Asp Asp Arg Asn
325 330

gga gac ttc tca gag aat aga gac tgt qac aag ctg gaa 1505
Gly Asp Phe Ser Glu Asn Arg Asp Cys Asp Lys Leu Glu
335 340 345

gat ttg gag gac aac agc aca cct gaa cca aag gaa aat 1544
Asp Leu Glu Asp Asn Ser Thr Pro Glu Pro Lys Glu Asn
350 355 360

ggg gag gaa ggc tgt cat caa aat ggt ctt gcc ctc cct 1583
Gly Glu Glu Gly Cys His Gln Asn Gly Leu Ala Leu Pro
365 370

gta gtg gaa gaa ggg gag gtt ctc tca cac tct cta gaa 1622
Val Val Glu Glu Gly Glu Val Leu Ser His Ser Leu Glu
375 380 385

gca gag cac agg tta ttg aaa gct atg ggt tgg cag gaa 1661
Ala Glu His Arg Leu Leu Lys Ala Met Gly Trp Gln Glu
390 395

tat cct gaa aat gat gag aat tgc ctt ccc ctc aca gag 1700
Tyr Pro Glu Asn Asp Glu Asn Cys Leu Pro Leu Thr Glu
400 405 410

gat gag ctc aaa gag ttc cac atg aag aca gag cag ctg 1739
Asp Glu Leu Lys Glu Phe His Met Lys Thr Glu Gln Leu
415 420 425

aga aga aat ggc ttt gga aag aat ggc ttc ttg cag agc 1778
Arg Arg Asn Gly Phe Gly Lys Asn Gly Phe Leu Gln Ser
430 435

cgc aqt tcc agt ctg ttc tcc cct tgg aga agc act tgc 1817
Arg Ser Ser Ser Leu Phe Ser Pro Trp Arg Ser Thr Cys
440 445 450

aaa gca gag ttt gag gac tca gac acc gaa acc agt agc 1856
Lys Ala Glu Phe Glu Asp Ser Asp Thr Glu Thr Ser Ser
455 460

agt gaa aca tca gat gac gat gcc tgg aag t agg 1890
Ser Glu Thr Ser Asp Asp Asp Ala Trp Lys
465 470 474

catataaaatq ctacacagtta aatctgaccc aataaactct gtgtgttttag 1940
ggagtataaca aaagaaaatcg ttcttttctt tttcttatgt tgttgaatac 1990
ttcattcaca agggaaataa tcataccca aagagagaaa aaaaaaaaaa 2040
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ataagcttgg ccgcataqqd ccaacttgt 2119

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20 25 30
Glu His Leu Pro Arg Gly Glu Gly Arg Phe Gly Val Ser Arg Arg 45
35 40 45
Arg His Asn Ser Ser Asp Gly Phe Phe Asn Asn Gly Pro Leu Arg 60
50 55 60
Thr Ala Gly Asp Ser Trp His Gln Pro Ser Cys Ser Ala Met Ile 75
65 70 75
Leu Trp Thr Leu Val Ser Leu Arg Glu His Met Leu Glu Ser Gln 90
80 85 90
Gly Thr His Leu Val Gly Ile Ala Leu Pro Arg Gly His Asp Gly 105
95 100 105
Met Ser Gln Arg Ser Val Gly Gly Thr Gly Asn His Arg His Trp 120
110 115 120
Asn Gly Ser Phe His Ser Arg Lys Gly Cys Ala Phe Gln Glu Lys 135
125 130 135
Pro Pro Met Glu Ile Arg Glu Glu Lys Lys Glu Asp Lys Val Glu 150
140 145 150
Lys Leu Gln Phe Glu Glu Glu Asp Phe Pro Ser Leu Asn Pro Glu 165
155 160 165
Ala Gly Lys Gln His Gln Pro Cys Arg Pro Ile Gly Thr Pro Ser 180
170 175 180
Gly Val Trp Glu Asn Pro Pro Ser Ala Lys Gln Pro Ser Lys Met 195
185 190 195
Leu Val Ile Lys Lys Val Ser Lys Glu Asp Pro Ala Ala Ala Phe 210
200 205 210
Ser Ala Ala Phe Thr Ser Pro Gly Ser His His Ala Asn Gly Asn 225
215 220 225

Lys Leu Ser Ser Val Val Pro Ser Val Tyr Lys Asn Leu Val Pro
 230 235 240
 Lys Pro Val Pro Pro Ser Lys Pro Asn Ala Trp Lys Ala Asn
 245 250 255
 Arg Met Glu His Lys Ser Gly Ser Leu Ser Ser Arg Glu Ser
 260 265 270
 Ala Phe Thr Ser Pro Ile Ser Val Thr Lys Pro Val Val Leu Ala
 275 280 285
 Ser Gly Ala Ala Leu Ser Ser Pro Lys Glu Ser Pro Ser Ser Thr
 290 295 300
 Thr Pro Pro Ile Glu Ile Ser Ser Ser Arg Leu Thr Lys Leu Thr
 305 310 315
 Arg Arg Thr Thr Asp Arg Lys Ser Glu Phe Leu Lys Thr Leu Lys
 320 325 330
 Asp Asp Arg Asn Gly Asp Phe Ser Glu Asn Arg Asp Cys Asp Lys
 335 340 345
 Leu Glu Asp Leu Glu Asp Asn Ser Thr Pro Glu Pro Lys Glu Asn
 350 355 360
 Gly Glu Glu Gly Cys His Gln Asn Gly Leu Ala Leu Pro Val Val
 365 370 375
 Glu Glu Gly Glu Val Leu Ser His Ser Leu Glu Ala Glu His Arg
 380 385 390
 Leu Leu Lys Ala Met Gly Trp Gln Glu Tyr Pro Glu Asn Asp Glu
 395 400 405
 Asn Cys Leu Pro Leu Thr Glu Asp Glu Leu Lys Glu Phe His Met
 410 415 420
 Lys Thr Glu Gln Leu Arg Arg Asn Gly Phe Gly Lys Asn Gly Phe
 425 430 435
 Leu Gln Ser Arg Ser Ser Leu Phe Ser Pro Trp Arg Ser Thr
 440 445 450
 Cys Lys Ala Glu Phe Glu Asp Ser Asp Thr Glu Thr Ser Ser Ser
 455 460 465
 Glu Thr Ser Asp Asp Asp Ala Trp Lys
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 <121> unsure
 <122> 162, 165, 183-184, 187, 204, 207, 211, 216, 219, 222-223, 225,
 237, 240, 244, 250, 253, 262, 267, 269, 275, 279, 282, 289-290
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auctggcaga tngtnagaag atacagtgc tttttatntgc ttaacaacag 200
c tncanatt ncaggncna gnntncctct tcctccnaan aaantgattn 250
ggnaacatgg ancgtqnant tcatngctng anaggcagnn aggt 294

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<211> unsure
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774, 784
<213> unknown base

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caaccctcca agatgtatgt tatcaaaaaa gtttccaaag aggatcctgc 200
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gaaacaaaatt gtcatccgtg gttccaagtg tctataaagaa cctggttcct 300
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tcaagttctnc ccaaagagag tccctccagc accaccctc cnaattgaga 500
ttagtcttc tcgtctngac caagtttgac ccggccgaacc naccgacang 550
gaagragtga ngttcctgaa aactnctgna anggatgacc ggaaatggga 600
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caacagcaca ctgaacccaa gaaaaatggg ggaggaaggc tgttcatcaa 700
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<212> DNA

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<210> 12

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<213> Homo sapiens

<400> 12

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<210> 13

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atgtatgtccc ttctctcacc atg agc tgg ctc tcc agt tcc 91

Met Ser Trp Leu Ser Ser Ser
1 5

cag gga gtg gtn cta aca gcc tac cac ccc agc qqc aag 130
Gln Gly Val Xaa Leu Thr Ala Tyr His Pro Ser Gly Lys
10 15 20

gac cag acc gtc qgg aac aq c cat gca aag gca ggg gag 169
Asp Gln Thr Val Gly Asn Ser His Ala Gly Glu
25 30

gaa gcc acc tcg agt cgc aga tat ggc cag tac act atg 208
Glu Ala Thr Ser Ser Arg Arg Tyr Gly Gln Tyr Thr Met
35 40 45

aac cag gaa agc acc acc atc aaa gtt atg gag aag cct 247
Asn Gln Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro
50 55

cca ttt gat cga tca att tcc cag gat tct ttg gat gaa 286
Pro Phe Asp Arg Ser Ile Ser Gln Asp Ser Leu Asp Glu
60 65 70

cta tct atg gaa gac tat tgg ata gaa cta gaa aac atc 325
Leu Ser Met Glu Asp Tyr Trp Ile Glu Leu Glu Asn Ile
75 80 85

aag aaa tct agt gaa aac agc caa gaa gat caa gag gtg 364
Lys Lys Ser Ser Glu Asn Ser Gln Glu Asp Gln Glu Val
90 95

gtt gtt gtc aaa gag cct gat gag gga gaa ttg gaa gaa 403
Val Val Val Lys Glu Pro Asp Glu Gly Glu Leu Glu Glu
100 105 110

gag tgg ctt aaa gag gcc ggt tta tcc aat ctc ttc gga 442
Glu Trp Leu Lys Glu Ala Gly Leu Ser Asn Leu Phe Gly
115 120

gag tct gct gga gat cca cag gaa agc att gtg ttt tta 481
Glu Ser Ala Gly Asp Pro Gln Glu Ser Ile Val Phe Leu
125 130 135

tca aca ttg acg cgg acc cag gca gca gca gtt cag aag 520
Ser Thr Leu Thr Arg Thr Gln Ala Ala Ala Val Gln Lys
140 145 150

cga gta gag acg gtc tcc cag acc ttg agg aaa aaa aac 559
Arg Val Glu Thr Val Ser Gln Thr Leu Arg Lys Lys Asn
155 160

aaa cag tac gag att cct gac gtc aga gac ata ttt gct 598
Lys Gln Tyr Gln Ile Pro Asp Val Arg Asp Ile Phe Ala
165 170 175

caa cag aga gaa tca aaa gaa aca gct cca ggt ggc act 637
Gln Gln Arg Glu Ser Lys Glu Thr Ala Pro Gly Gly Thr
180 185

gaa tcg cag tca ctt aga aca aat gaa aac aaa tac caa 676
Glu Ser Gln Ser Leu Arg Thr Asn Glu Asn Lys Tyr Gln

190

195

200

gga aga gat gac gag gca tct aac ctt gtt ggt gaa gag 715
 Gly Arg Asp Asp Glu Ala Ser Asn Leu Val Gly Glu Glu
 205 210 215

aag ctg atc cca cct gag qaq acg cct gcc cct gaa aca 754
 Lys Leu Ile Pro Pro Glu Glu Thr Pro Ala Pro Glu Thr
 220 225

gac atc aac ctg gag gta tca ttt gcc gag caa qca ctc 793
 Asp Ile Asn Leu Glu Val Ser Phe Ala Glu Gln Ala Leu
 230 235 240

aat cag aaa gag aga tcc aag gag aaa atc cag aag agc 832
 Asn Gln Lys Glu Arg Ser Lys Glu Lys Ile Gln Lys Ser
 245 250

aaa ggc gat gat gcc aca tta cct agt ttc aga ttg cca 871
 Lys Gly Asp Asp Ala Thr Leu Pro Ser Phe Arg Leu Pro
 255 260 265

aaa gac aaa acg ggt acc aca agg att ggt gac ctc gca 910
 Lys Asp Lys Thr Gly Thr Arg Ile Gly Asp Leu Ala
 270 275 280

ccc cag gac atg aag aaa gtt tgc cat tta gcc cta att 949
 Pro Gln Asp Met Lys Lys Val Cys His Leu Ala Leu Ile
 285 290

gag ctg act gcc ctc tat gat gta ttg ggt att gag ctg 988
 Glu Leu Thr Ala Leu Tyr Asp Val Leu Gly Ile Glu Leu
 295 300 305

aaa caa caa aaa gct gtg aaa atc aaa aca aaa gat tct 1027
 Lys Gln Gln Lys Ala Val Lys Ile Lys Thr Lys Asp Ser
 310 315

ggc ctt ttt tgc gtt cca ttg aca gcg cta tta gaa caa 1066
 Gly Leu Phe Cys Val Pro Leu Thr Ala Leu Leu Glu Gln
 320 325 330

gat cag agg aaa gta cca gga atg cga ata ccc ttg atc 1105
 Asp Gln Arg Lys Val Pro Gly Met Arg Ile Pro Leu Ile
 335 340 345

ttt caa aaa ctg att tct cga att gaa gag aga ggt ttg 1144
 Phe Gln Lys Leu Ile Ser Arg Ile Glu Glu Arg Gly Leu
 350 355

gaa aca gaa ggc ctc tta cgg atc cct gga gct gcc att 1183
 Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly Ala Ala Ile
 360 365 370

aga atc aag aat ctt tgc caa gaa cta gaa gca aag ttt 1222
 Arg Ile Lys Asn Leu Cys Gln Glu Leu Glu Ala Lys Phe
 375 380

tat gaa ggg act ttt aat tgg gaa agt gtc aaa cag cat 1261
 Tyr Glu Gly Thr Phe Asn Trp Glu Ser Val Lys Gln His
 385 390 395

gat gcc gcc agc ctg ctg aag ctc ttc att cgg gag ttg 1300
Asp Ala Ala Ser Leu Leu Lys Leu Phe Ile Arg Glu Leu
400 405 410

ccc cag cca ctg ctc aqt gtg gag tat ctc aaa gcc ttt 1339
Pro Gln Pro Leu Leu Ser Val Glu Tyr Leu Lys Ala Phe
415 420

cag gct gtc cag aat ctt cca acc aag aag cag caa cta 1378
Gln Ala Val Gln Asn Leu Pro Thr Lys Lys Gln Gln Leu
425 430 435

cag gct ttg aac ctt ctt gtc atc ctc cta cct gat gca 1417
Gln Ala Leu Asn Leu Leu Val Ile Leu Leu Pro Asp Ala
440 445

aac agg gac aca ctg aag gcc ctt ctt gaa ttt ctc caa 1456
Asn Arg Asp Thr Leu Lys Ala Leu Leu Glu Phe Leu Gln
450 455 460

aga gta ata gat aat aaa gaa aaa aat aaa atg aca gtc 1495
Arg Val Ile Asp Asn Lys Glu Lys Asn Lys Met Thr Val
465 470 475

atg aat gta gca atg gtc atg gcc ccg aat ctc ttt atg 1534
Met Asn Val Ala Met Val Met Ala Pro Asn Leu Phe Met
480 485

tgt cat gca ttg gga ttg aag tcc agt gaa cag cga gaa 1573
Cys His Ala Leu Gly Leu Lys Ser Ser Glu Gln Arg Glu
490 495 500

ttt gta atg gca gct ggg aca gca aat acc atg cac tta 1612
Phe Val Met Ala Ala Gly Thr Ala Asn Thr Met His Leu
505 510

ttg att aag tac caa aaa ctt ctg tgg aca att ccc aag 1651
Leu Ile Lys Tyr Gln Lys Leu Leu Trp Thr Ile Pro Lys
515 520 525

ttt att gta aac caa gtg agg aag caa aac acg gaa aat 1690
Phe Ile Val Asn Gln Val Arg Lys Gln Asn Thr Glu Asn
530 535 540

cat aaa aag gat aaa aga gcc atg aag aaa ttg ctg aag 1729
His Lys Lys Asp Lys Arg Ala Met Lys Lys Leu Leu Lys
545 550

aaa atg gct tat gac cga gaa aaa tat gaa aag caa gat 1768
Lys Met Ala Tyr Asp Arg Glu Lys Tyr Glu Lys Gln Asp
555 560 565

aag agt aca aat gat gct gac gtt cct cag gga gtg att 1807
Lys Ser Thr Asn Asp Ala Asp Val Pro Gln Gly Val Ile
570 575

cga gtg caa gct ccc cat ctt tcg aaa gtt tcc atg gca 1846
Arg Val Gln Ala Pro His Leu Ser Lys Val Ser Met Ala
580 585 590

ata cag cta act gaa gaa cta aaa gcc agt gat gta ctt 1885
Ile Gln Leu Thr Glu Glu Leu Lys Ala Ser Asp Val Leu
595 600 605

gcc agg ttt ctc agc caa gaa agt ggg gtt gcc cag act 1924
Ala Arg Phe Leu Ser Gln Glu Ser Gly Val Ala Gln Thr
610 615

ctc aag aaa gga gaa gtt ttt ttg tat gaa att gga gga 1963
Leu Lys Lys Gly Glu Val Phe Leu Tyr Glu Ile Gly Gly
620 625 630

aat att ggg gaa cgc tgc ctt gat gat gac act tac atg 2002
Asn Ile Gly Glu Arg Cys Leu Asp Asp Asp Thr Tyr Met
635 640

aag gat tta tat cag ctt aac cca aat gct gag tgg gtt 2041
Lys Asp Leu Tyr Gln Leu Asn Pro Asn Ala Glu Trp Val
645 650 655

ata aag tca aag cca ttg t agaagactta acaagctgca 2080
Ile Lys Ser Lys Pro Leu
660 663

gataaccatg tggacttctg tcataattct tgctgagtca agagtgtaaa 2130
taaaagaaat ggccaggactc atattattca gttgtaccca agtattttaa 2180
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attatattaa attattatta atggtattat tagaaaaaaaaa aatttctgga 2280
gtgagagtaa agaggctaa ttagtttgtg ggcagtttc ttatgctctg 2330
tgaaatgtgt ccagatgtga catagtttt tttttt 2366

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Ala Gly Glu Ala Thr Ser Ser Arg Arg Tyr Gly Gln Tyr Thr
35 40 45

Met Asn Gln Glu Ser Thr Thr Ile Lys Val Met Glu Lys Pro Pro
50 55 60

Phe Asp Arg Ser Ile Ser Gln Asp Ser Leu Asp Glu Leu Ser Met
65 70 75

Glu Asp Tyr Trp Ile Glu Leu Glu Asn Ile Lys Lys Ser Ser Glu
80 85 90

Asn Ser Gln Glu Asp Gln Glu Val Val Val Lys Glu Pro Asp

95	105	105
Glu	Gly	
Glu	Glu	
Leu	Glu	
Glu	Glu	
Trp	Leu	Lys
		Glu
110		Ala
		Gly
		Leu
		Ser
Asn	Leu	
Phe	Gly	
Glu	Ser	
Ala	Gly	
Asp	Pro	Gln
		Glu
		Ser
Ile	Val	
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		115
Phe	Leu	Ser
Thr	Leu	Thr
Arg	Thr	Gln
		Ala
		Ala
		Ala
		Val
		Gln
		Lys
140		
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Arg	Val	Glu
Val	Glu	Thr
		Val
		Ser
		Gln
		Thr
		Leu
		Arg
		Lys
		Lys
		Asn
		Lys
155		
		160
Tyr	Gln	Ile
		Pro
		Asp
		Val
		Arg
		Asp
		Ile
		Phe
		Ala
		Gln
		Arg
		Glu
170		
		175
Ser	Lys	Glu
		Thr
		Ala
		Pro
		Gly
		Gly
		Thr
		Glu
		Ser
		Gln
		Ser
		Leu
		Arg
185		
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Thr	Asn	Glu
		Asn
		Lys
		Tyr
		Gln
		Gly
		Arg
		Asp
		Asp
		Glu
		Ala
		Ser
		Asn
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Leu	Val	Gly
		Glu
		Glu
		Lys
		Leu
		Ile
		Pro
		Pro
		Glu
		Glu
		Thr
		Pro
		Ala
215		
		220
Pro	Glu	Thr
		Asp
		Ile
		Asn
		Leu
		Glu
		Val
		Ser
		Phe
		Ala
		Glu
		Gln
230		
		235
Leu	Asn	Gln
		Lys
		Glu
		Arg
		Ser
		Lys
		Glu
		Ile
		Gln
		Lys
245		
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Gly	Asp	Asp
		Ala
		Thr
		Leu
		Pro
		Ser
		Phe
		Arg
		Leu
		Pro
		Lys
260		
		265
Thr	Gly	Thr
		Arg
		Ile
		Gly
		Asp
		Leu
		Ala
		Pro
		Gln
		Asp
		Met
		Lys
275		
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Lys	Val	Cys
		His
		Leu
		Ala
		Ile
		Glu
		Leu
		Thr
		Ala
		Leu
		Tyr
		Asp
290		
		295
val	Leu	Gly
		Ile
		Glu
		Leu
		Lys
		Gln
		Gln
		Lys
		Ala
		Val
		Lys
		Ile
		Lys
305		
		310
Thr	Lys	Asp
		Ser
		Gly
		Leu
		Phe
		Cys
		Val
		Pro
		Leu
		Thr
		Ala
		Leu
		Leu
320		
		325
Glu	Gln	Asp
		Gln
		Arg
		Lys
		Val
		Pro
		Gly
		Met
		Arg
		Ile
		Pro
		Leu
		Ile
335		
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Phe	Gln	Lys
		Leu
		Ile
		Ser
		Arg
		Ile
		Glu
		Glu
		Arg
		Gly
		Leu
		Glu
		Thr
		Pro
		Ala
		Leu
		Leu
		Arg
		Ile
		Pro
		Gly
		Ala
		Ala
		Ile
		Arg
		Ile
		Lys
		Asn
365		
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Leu	Cys	Gln
		Glu
		Leu
		Glu
		Ala
		Lys
		Phe
		Tyr
		Glu
		Gly
		Thr
		Phe
		Asn
380		
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Trp	Glu	Ser
		Val
		Lys
		Gln
		His
		Asp
		Ala
		Ala
		Ser
		Leu
		Leu
		Lys
395		
		400

Phe Ile Arg Glu Leu Pro Gln Pro Leu Leu Ser Val Glu Tyr Leu
 410 415 420
 Lys Ala Phe Gln Ala Val Gln Asn Leu Pro Thr Lys Lys Gln Gln
 425 430 435
 Leu Gln Ala Leu Asn Leu Leu Val Ile Leu Leu Pro Asp Ala Asn
 440 445 450
 Arg Asp Thr Leu Lys Ala Leu Leu Glu Phe Leu Gln Arg Val Ile
 455 460 465
 Asp Asn Lys Glu Lys Asn Lys Met Thr Val Met Asn Val Ala Met
 470 475 480
 Val Met Ala Pro Asn Leu Phe Met Cys His Ala Leu Gly Leu Lys
 485 490 495
 Ser Ser Glu Gln Arg Glu Phe Val Met Ala Ala Gly Thr Ala Asn
 500 505 510
 Thr Met His Leu Leu Ile Lys Tyr Gln Lys Leu Leu Trp Thr Ile
 515 520 525
 Pro Lys Phe Ile Val Asn Gln Val Arg Lys Gln Asn Thr Glu Asn
 530 535 540
 His Lys Lys Asp Lys Arg Ala Met Lys Lys Leu Leu Lys Lys Met
 545 550 555
 Ala Tyr Asp Arg Glu Lys Tyr Glu Lys Gln Asp Lys Ser Thr Asn
 560 565 570
 Asp Ala Asp Val Pro Gln Gly Val Ile Arg Val Gln Ala Pro His
 575 580 585
 Leu Ser Lys Val Ser Met Ala Ile Gln Leu Thr Glu Glu Leu Lys
 590 595 600
 Ala Ser Asp Val Leu Ala Arg Phe Leu Ser Gln Glu Ser Gly Val
 605 610 615
 Ala Gln Thr Leu Lys Lys Gly Glu Val Phe Leu Tyr Glu Ile Gly
 620 625 630
 Gly Asn Ile Gly Glu Arg Cys Leu Asp Asp Asp Thr Tyr Met Lys
 635 640 645
 Asp Leu Tyr Gln Leu Asn Pro Asn Ala Glu Trp Val Ile Lys Ser
 650 655 660
 Lys Pro Leu

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 <212> DNA
 <213> Homo sapiens

<220>

<221> unsure
<222> 74, 1306
<223> unknown base

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gacccagggc ccggcactg cctngtgtga ggggctggca gtttccaa 100
tgcaagcaagt ggaggcccct gcagcttcg ggcctgtggg caggggcata 150
gtggggcagg qqtgtggctq cccgccccgg caagctgca cctgtctct 200
cttgtgacc agtaccccaa ggggatcats tggggatccq tctgcagga 250
cctgtgtgag ctgcat atg gtg gag tgg agg acc tgc ctc 290
Met Val Glu Trp Arg Thr Cys Leu
1 5

tgc gtg gcc ccg ggc cag cag gtg tac agc ggg ctc tgg 329
Ser Val Ala Pro Gly Gln Gln Val Tyr Ser Gly Leu Trp
10 15 20

cgg gac aag gat gta acc atc aag tgt ggc att gag gag 368
Arg Asp Lys Asp Val Thr Ile Lys Cys Gly Ile Glu Glu
25 30

acc ctc gac tcc aag gcc cggtcg gat gcg gcc ccc cgg 407
Thr Leu Asp Ser Lys Ala Arg Ser Asp Ala Ala Pro Arg
35 40 45

cggtcg gta ctg ttt gac aag ccc acc cgg ggc acc 446
Arg Glu Leu Val Leu Phe Asp Lys Pro Thr Arg Gly Thr
50 55 60

tcc atc aag gaa ttc cgg gag atg acc ctc ggc ttc ctc 485
Ser Ile Lys Glu Phe Arg Glu Met Thr Leu Gly Phe Leu
65 70

aag gcg aac ctg gga gac ctg cct tcc ctg ccg gcg ctg 524
Lys Ala Asn Leu Gly Asp Leu Pro Ser Leu Pro Ala Leu
75 80 85

gtt ggc cag gtc ctg ctc atg gct gac ttc aac aag gac 563
Val Gly Gln Val Leu Leu Met Ala Asp Phe Asn Lys Asp
90 95

aac cgg gtc tcc ctg qcg gaa gcc aag tcc gtg tgg gcc 602
Asn Arg Val Ser Leu Ala Glu Ala Lys Ser Val Trp Ala
100 105 110

ctg ctg cag cgt aac qaq ttc ctg ctg ctg tcc ctg 641
Leu Leu Gln Arg Asn Glu Phe Leu Leu Leu Ser Leu
115 120 125

caq qag aag gag cac gcc tcc aga ctg ctg ggc tac tgt 680
Gln Glu Lys Glu His Ala Ser Arg Leu Leu Gly Tyr Cys
130 135

ggg gac ctc tac ctc acc gag ggc gtg ccg cat ggc gcc 719
Gly Asp Leu Tyr Leu Thr Glu Gly Val Pro His Gly Ala

140

145

150

tgg cac gcg gcc gcc ctc cca ccc ctg ttg cgc cca ctg 758
 Trp His Ala Ala Ala Leu Pro Pro Leu Leu Arg Pro Leu
 155 160

ctg ccc cct gcc ctg cag ggt gct ctc caq caq tgg ctg 797
 Leu Pro Pro Ala Leu Gln Gly Ala Leu Gln Gln Trp Leu
 165 170 175

agg cct gcg tgg cct tgg cgg gcc aag atc gcc atc ggc 836
 Gly Pro Ala Trp Pro Trp Arg Ala Lys Ile Ala Ile Gly
 180 185 190

ctg ctg gag ttc gtg gag gag ctc ttc cac ggc tct tac 875
 Leu Leu Glu Phe Val Glu Glu Leu Phe His Gly Ser Tyr
 195 200

ggg act ttc tac atg tgt gag acc aca ctg gcc aac gtg 914
 Gly Thr Phe Tyr Met Cys Glu Thr Thr Leu Ala Asn Val
 205 210 215

ggc tac aca gcc acc tac gac ttc aag atg gcc gac ctg 953
 Gly Tyr Thr Ala Thr Tyr Asp Phe Lys Met Ala Asp Leu
 220 225

cag cag gtg gca ccc gag gcc acc gtg cgc cgc ttc ctg 992
 Gln Gln Val Ala Pro Glu Ala Thr Val Arg Arg Phe Leu
 230 235 240

cag ggc cgc cgc tgc gag cac agc acc gac tgc acc tac 1031
 Gln Gly Arg Arg Cys Glu His Ser Thr Asp Cys Thr Tyr
 245 250 255

ggg cgc gac tgc agg gcc ccg tgt gac agg ctc atg agg 1070
 Gly Arg Asp Cys Arg Ala Pro Cys Asp Arg Leu Met Arg
 260 265

cag tgc aag ggc gac ctc atc cag ccc aac ctg gcc aag 1109
 Gln Cys Lys Gly Asp Leu Ile Gln Pro Asn Leu Ala Lys
 270 275 280

gtg tgc gca ctg cta cgg ggc tac ctg ctg cct ggc gcg 1148
 Val Cys Ala Leu Leu Arg Gly Tyr Leu Leu Pro Gly Ala
 285 290

ccc gcc qac ctc cgc gag gag ctg ggc aca cag ctg cgc 1187
 Pro Ala Asp Leu Arg Glu Glu Leu Gly Thr Gln Leu Arg
 295 300 305

acc tgt acc acg ctg agc ggg ctg ggc agc cag gtg gag 1226
 Thr Cys Thr Thr Leu Ser Gly Leu Ala Ser Gln Val Glu
 310 315 320

gcc cat cac tgg ctg gtg ctc agc cac ctc aag act ctg 1265
 Ala His His Ser Leu Val Leu Ser His Leu Lys Thr Leu
 325 330

ctc tgg aag aag atc tcc aac acc aag tac tct t g 1300
 Leu Trp Lys Lys Ile Ser Asn Thr Lys Tyr Ser
 335 340 344

atgggnaatg agggcttgca accttct 1327

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<211> 344

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 104

<223> unknown amino acid

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Gly Ile Glu Glu Thr Leu Asp Ser Lys Ala Arg Ser Asp Ala Ala
35 40 45

Pro Arg Arg Glu Leu Val Leu Phe Asp Lys Pro Thr Arg Gly Thr
50 55 60

Ser Ile Lys Glu Phe Arg Glu Met Thr Leu Gly Phe Leu Lys Ala
65 70 75

Asn Leu Gly Asp Leu Pro Ser Leu Pro Ala Leu Val Gly Gln Val
80 85 90

Leu Leu Met Ala Asp Phe Asn Lys Asp Asn Arg Val Ser Xaa Ala
95 100 105

Glu Ala Lys Ser Val Trp Ala Leu Leu Gln Arg Asn Glu Phe Leu
110 115 120

Leu Leu Leu Ser Leu Gln Glu Lys Glu His Ala Ser Arg Leu Leu
125 130 135

Gly Tyr Cys Gly Asp Leu Tyr Leu Thr Glu Gly Val Pro His Gly
140 145 150

Ala Trp His Ala Ala Ala Leu Pro Pro Leu Leu Arg Pro Leu Leu
155 160 165

Fro Pro Ala Leu Gln Gly Ala Leu Gln Gln Trp Leu Gly Pro Ala
170 175 180

Trp Pro Trp Arg Ala Lys Ile Ala Ile Gly Leu Leu Glu Phe Val
185 190 195

Glu Glu Leu Phe His Gly Ser Tyr Gly Thr Phe Tyr Met Cys Glu
200 205 210

Thr Thr Leu Ala Asn Val Gly Tyr Thr Ala Thr Tyr Asp Phe Lys
215 220 225

Met Ala Asp Leu Gln Gln Val Ala Pro Glu Ala Thr Val Arg Arg
230 235 240

Phe Leu Gln Gly Arg Arg Cys Glu His Ser Thr Asp Cys Thr Tyr
 245 250 255
 Gly Arg Asp Cys Arg Ala Pro Cys Asp Arg Leu Met Arg Gln Cys
 260 265 270
 Lys Gly Asp Leu Ile Gln Pro Asn Leu Ala Lys Val Cys Ala Leu
 275 280 285
 Leu Arg Gly Tyr Leu Leu Pro Gly Ala Pro Ala Asp Leu Arg Glu
 290 295 300
 Glu Leu Gly Thr Gln Leu Arg Thr Cys Thr Thr Leu Ser Gly Leu
 305 310 315
 Ala Ser Gln Val Glu Ala His His Ser Leu Val Leu Ser His Leu
 320 325 330
 Lys Thr Leu Leu Trp Lys Lys Ile Ser Asn Thr Lys Tyr Ser
 335 340

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<220>
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 <222> 4, 107, 109, 112, 119, 122, 176, 323, 1616, 1878, 1881, 1911,
 1924, 1939, 1953, 1982, 1991-1992, 2000, 2443
 <223> unknown base

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 tgctctngng cnccggcaant cnccggagct actgcaccag gggcgctacc 150
 aggagccctg gcccgcctg cgaggncgtc gagcagaacc cagtgacttg 200
 attgtaaaaa ttacagagc ggaatcatat gctggcttcc aagagttaa 250
 agcagccctta gaagattaa atg cag ttc ttt ttc aac ttc 291
 Met Gln Phe Phe Phe Asn Phe
 1 5

caa gat tgg cct gaa ggt cta ctt cag gaa ang gaa aaa 330
 Gln Asp Trp Pro Glu Gly Leu Leu Gln Glu Xaa Glu Lys
 10 15 20

gta ctc tgc gat gct ttt tta ggt gat gcc tta caa 369
 Val Leu Cys Asp Ala Gly Phe Leu Gly Asp Ala Leu Gln
 25 30

ctc ttt ctt cag tgc tta gcc ctt gat gaa gat ttt gca 408
 Leu Phe Leu Gln Cys Leu Ala Leu Asp Glu Asp Phe Ala
 35 40 45

ctc gca aag ctg caa gta caa aag att tta tgt gat tta 447

Pro Ala Lys Leu Gln Val Gln Lys Ile Leu Cys Asp Leu
50 55

tta tta cct gaa aac tta aaa gaa ggc ctg aag gaa tot 486
Leu Leu Pro Glu Asn Leu Lys Glu Gly Leu Lys Glu Ser
60 65 70

tcc tgg agt tca tta cca tgt act aaa aac aga cct ttt 525
Ser Trp Ser Ser Leu Pro Cys Thr Lys Asn Arg Pro Phe
75 80 85

gat ttt cat tca gtg atg gaa gag tct cag ttc aat 564
Asp Phe His Ser Val Met Glu Glu Ser Gln Ser Leu Asn
90 95

gaa cct agc cca aag cag agt gaa qaa ata cca gag gtc 603
Glu Pro Ser Pro Lys Gln Ser Glu Glu Ile Pro Glu Val
100 105 110

act tca gag cct gtc aaa gga agc tta aac cgt gct cag 642
Thr Ser Glu Pro Val Lys Gly Ser Leu Asn Arg Ala Gln
115 120

tca gca cag tct ata aat tca aca gaa atg cct gcc aga 681
Ser Ala Gln Ser Ile Asn Ser Thr Glu Met Pro Ala Arg
125 130 135

gag gac tgt tta aaa aaa gtg tcc tca gaa cct gtt ctg 720
Glu Asp Cys Leu Lys Val Ser Ser Glu Pro Val Leu
140 145 150

tca gtt caa gaa aaa ggt gtt ctg ctg aaa aga aag ttg 759
Ser Val Gln Glu Lys Gly Val Leu Leu Lys Arg Lys Leu
155 160

tct ctt tta gaa cag gat gtg att gta aat gaa gat gga 798
Ser Leu Leu Glu Gln Asp Val Ile Val Asn Glu Asp Gly
165 170 175

aga aat aag ctg aaa aaa caa gga gaa act ccc aat gaa 837
Arg Asn Lys Leu Lys Gln Gly Glu Thr Pro Asn Glu
180 185

gtc tgt atg ttt tcc tta gct tat qgt gat att cca gaa 876
Val Cys Met Phe Ser Leu Ala Tyr Gly Asp Ile Pro Glu
190 195 200

gaa tta atc gat gtc tca gat ttc gag tgt tct ctc tgc 915
Glu Leu Ile Asp Val Ser Asp Phe Glu Cys Ser Leu Cys
205 210 215

atg agg ttg ttt ttt gag cca gta aca acc cct tgc qqa 954
Met Arg Leu Phe Phe Glu Pro Val Thr Thr Pro Cys Gly
220 225

cat tcg ttc tgt aag aat tgt ctt gag cgt tgt tta gat 993
His Ser Phe Cys Lys Asn Cys Leu Glu Arg Cys Leu Asp
230 235 240

cat gca cca tat tgt cct ctt tgc aaa gaa agc tta aat 1032
His Ala Pro Tyr Cys Pro Leu Cys Lys Glu Ser Leu Asn

245

250

gag tat cta gca gat agg agg tac tqt qtc aca cag ctg 1071
 Glu Tyr Leu Ala Asp Arg Arg Tyr Cys Val Thr Gln Leu
 255 260 265

ttg qaa gaa tta ata gtg aag tat ctg cct gat gaa ctg 1110
 Leu Glu Glu Leu Ile Val Lys Tyr Leu Pro Asp Glu Leu
 270 275 280

tct gag aqa aaa aaa ata tat gaa gaa gaa act qct gaa 1149
 Ser Glu Arg Lys Lys Ile Tyr Glu Glu Glu Thr Ala Glu
 285 290

ctc tca cac ttg acc aag aat gtt cca ata ttt gtt tgc 1188
 Leu Ser His Leu Thr Lys Asn Val Pro Ile Phe Val Cys
 295 300 305

act atg gcc tac ccc act gtg cct tgc cct ctc cat gta 1227
 Thr Met Ala Tyr Pro Thr Val Pro Cys Pro Leu His Val
 310 315

ttt gag cca aga tac aga ttg atg att cga aga agt ata 1265
 Phe Glu Pro Arg Tyr Arg Leu Met Ile Arg Arg Ser Ile
 320 325 330

cag act gga acc aaa cag ttt ggc atg tgt gtc agt gat 1305
 Gln Thr Gly Thr Lys Gln Phe Gly Met Cys Val Ser Asp
 335 340 345

aca caa aat agt ttt gca gat tat ggt tgt atq tta caa 1344
 Thr Gln Asn Ser Phe Ala Asp Tyr Gly Cys Met Leu Gln
 350 355

att aga aac gtg cat ttc tta ccg gac gga agg tct gtg 1383
 Ile Arg Asn Val His Phe Leu Pro Asp Gly Arg Ser Val
 360 365 370

gtt gat aca gtt gga gga aag cgg ttt agg gtt tta aaa 1422
 Val Asp Thr Val Gly Gly Lys Arg Phe Arg Val Leu Lys
 375 380

aga gga atg aaa gat gga tat tgc act gcc gac att gaa 1461
 Arg Gly Met Lys Asp Gly Tyr Cys Thr Ala Asp Ile Glu
 385 390 395

tat ctg gaa gat gtt aag gtt gag aat gaa gat gag att 1500
 Tyr Leu Glu Asp Val Lys Val Glu Asn Glu Asp Glu Ile
 400 405 410

aag aat ctc aga gag ctt cat gat ttg gtt tac tct caa 1539
 Lys Asn Leu Arg Glu Leu His Asp Leu Val Tyr Ser Gln
 415 420

gcc tgc agc tgg ttt cag aat tta aga gac aga ttt cga 1578
 Ala Cys Ser Trp Phe Gln Asn Leu Arg Asp Arg Phe Arg
 425 430 435

agc caa att ctt cag cat ttc gga tca atg ccc gag ang 1617
 Ser Gln Ile Leu Gln His Phe Gly Ser Met Pro Glu Xaa
 440 445

gag gaa aac ctt cag gca gcc cct aat qga cct gca tgg 1656
Glu Glu Asn Leu Gln Ala Ala Pro Asn Gly Pro Ala Trp
455 460

tgt tgg tgg ctt ctt gca gtt ctc cct gta gac cca cga 1695
Cys Trp Trp Leu Leu Ala Val Leu Pro Val Asp Pro Arg
465 470 475

tac cag ctg tcg gtt ttg tca atg aag tct ttg aaa gaa 1734
Tyr Gln Leu Ser Val Leu Ser Met Lys Ser Leu Lys Glu
480 485

cggttgc acc aag ata cag cat ata ctg acc tat ttt tct 1773
Arg Leu Thr Lys Ile Gln His Ile Leu Thr Tyr Phe Ser
490 495 500

aga gac caa tct aag t a actaactctt tggatctccc 1810
Arg Asp Gln Ser Lys
505 506

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<222> 18, 448
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Ala Leu Gln Leu Phe Leu Gln Cys Leu Ala Leu Asp Glu Asp Phe
35 40 45
Ala Pro Ala Lys Leu Gln Val Gln Lys Ile Leu Cys Asp Leu Leu
50 55 60
Leu Pro Glu Asn Leu Lys Glu Gly Leu Lys Glu Ser Ser Trp Ser
65 70 75
Ser Leu Pro Cys Thr Lys Asn Arg Pro Phe Asp Phe His Ser Val
80 85 90
Met Glu Glu Ser Gln Ser Leu Asn Glu Pro Ser Pro Lys Gln Ser
95 100 105
Glu Glu Ile Pro Glu Val Thr Ser Glu Pro Val Lys Gly Ser Leu
110 115 120
Asn Arg Ala Gln Ser Ala Gln Ser Ile Asn Ser Thr Glu Met Pro
125 130 135
Ala Arg Glu Asp Cys Leu Lys Lys Val Ser Ser Glu Pro Val Leu
140 145 150
Ser Val Gln Glu Lys Gly Val Leu Leu Lys Arg Lys Leu Ser Leu
155 160 165
Leu Glu Gln Asp Val Ile Val Asn Glu Asp Gly Arg Asn Lys Leu
170 175 180
Lys Lys Gln Gly Glu Thr Pro Asn Glu Val Cys Met Phe Ser Leu
185 190 195
Ala Tyr Gly Asp Ile Pro Glu Glu Leu Ile Asp Val Ser Asp Phe

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Pro Cys Gly His Ser Phe Cys Lys Asn Cys	Leu Glu Arg Cys Leu	
230	235	240
Asp His Ala Pro Tyr Cys Pro Leu Cys Lys	Glu Ser Leu Asn Glu	
245	250	255
Tyr Leu Ala Asp Arg Arg Tyr Cys Val Thr Gln	Leu Leu Glu Glu	
260	265	270
Leu Ile Val Lys Tyr Leu Pro Asp Glu	Leu Ser Glu Arg Lys Lys	
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Ile Tyr Glu Glu Glu Thr Ala Glu Leu Ser	His Leu Thr Lys Asn	
290	295	300
Val Pro Ile Phe Val Cys Thr Met Ala Tyr	Pro Thr Val Pro Cys	
305	310	315
Pro Leu His Val Phe Glu Pro Arg Tyr Arg	Leu Met Ile Arg Arg	
320	325	330
Ser Ile Gln Thr Gly Thr Lys Gln Phe	Gly Met Cys Val Ser Asp	
335	340	345
Thr Gln Asn Ser Phe Ala Asp Tyr Gly Cys	Met Leu Gln Ile Arg	
350	355	360
Asn Val His Phe Leu Pro Asp Gly Arg Ser	Val Val Asp Thr Val	
365	370	375
Gly Gly Lys Arg Phe Arg Val Leu Lys Arg	Gly Met Lys Asp Gly	
380	385	390
Tyr Cys Thr Ala Asp Ile Glu Tyr Leu Glu	Asp Val Lys Val Glu	
395	400	405
Asn Glu Asp Glu Ile Lys Asn Leu Arg Glu	Leu His Asp Leu Val	
410	415	420
Tyr Ser Gln Ala Cys Ser Trp Phe Gln Asn	Leu Arg Asp Arg Phe	
425	430	435
Arg Ser Gln Ile Leu Gln His Phe Gly Ser	Met Pro Xaa Arg Glu	
440	445	450
Glu Asn Leu Gln Ala Ala Pro Asn Gly	Pro Ala Trp Cys Trp Trp	
455	460	465
Leu Leu Ala Val Leu Pro Val Asp Pro Arg	Tyr Gln Leu Ser Val	
470	475	480
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Ile Leu Thr Tyr Phe Ser Arg Asp Gln Ser	Lys	
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tcaagtgtgg a gtatctaaa gccttcagg ctgtccagaa tttccaacc 200
aagaaggcgc aactacaggg ctttgaacc ctttcttta ctcattcctg 250
atgtttgata cccctgggtg aaaacaattc agtaaagcat cctgcctcan 300
acccccc 310

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<400> 20
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<210> 22
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<210> 24

<211> 533
<212> DNA
<213> Homo sapiens

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cagtcacaaa tttgcaacaa ataattacaa aagtttctaq ggcatgc 150
atataaacca tggcaqca tggtgatcta actgtgatat gaataaggca 200
taactaacat ttgcaccgag accagaatta aaaacaaaaaa caaactttaa 250
aagttagtt ctatattaaa cttcttctt tttccagat ccttaatggg 300
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attacacaaa tggcagttt atgtgaaaag ccccctaaaa tgtacaaact 400
aactggtaact gaattgagtt ctccctttac ctatgtac aattaaatgt 450
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aggaagccga gggtcatctc ccggattcc ttgatggagg tgccccgggt 200
gggcttgtca aacagtacca gtcggcccg gggggccgcat ccgaccgggc 250
cttggagtcg agggtctctt caatgccaca cttgatgggtt acatccttgt 300
cccgccagag cccgctgtac acctgctggc ccggggcaca cgagaagcag 350
ctcctccact ccaccatatg cagctcacac aggtctggc agacggagcc 400
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<400> 26
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atgggtggagt ggaggacctg 20

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PRO-C-MG.12	SEQ ID 3	SEQ ID 4
PRO-C-MG.45	SEQ ID 17	SEQ ID 18
PRO-C-MG.64	SEQ ID 15	SEQ ID 16
PRO-C-MG.72	SEQ ID 13	SEQ ID 14

2 May 15